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SEQUENCE LISTING

TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Yasuaki Ito
Ryo Fujii

(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/461,436
(B) FILING DATE: 14-DECEMBER-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513,974
(B) FILING DATE: 14-SEP-1995

(A) APPLICATION NUMBER: PCT/JP95/01599
(B) FILING DATE: 10-AUG-1995

(A) APPLICATION NUMBER: 7-093989
(B) FILING DATE: 19-APR-1995

(A) APPLICATION NUMBER: 7-057186
(B) FILING DATE: 16-MAR-1995

(A) APPLICATION NUMBER: 7-007177
(B) FILING DATE: 20-JAN-1995

(A) APPLICATION NUMBER: 6-326611
(B) FILING DATE: 28-DEC-1994

(A) APPLICATION NUMBER: 6-270017
(B) FILING DATE: 02-NOV-1994

(A) APPLICATION NUMBER: 6-236357

(B) FILING DATE: 30-SEP-1994

(A) APPLICATION NUMBER: 6-236356
(B) FILING DATE: 30-SEP-1994

(A) APPLICATION NUMBER: 6-189274
(B) FILING DATE: 11-AUG-1994

(A) APPLICATION NUMBER: 6-189273
(B) FILING DATE: 11-AUG-1994

(A) APPLICATION NUMBER: 6-189272
(B) FILING DATE: 11-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-439-4444
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGGCAACN YCCTG 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTNGWRRGGC ANCCAGCAGA KGGCAA

27

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCGCSGCYM TNRGYATGGA YCGNTAT 27

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATGTRGWAG GGAANCCAGS AMANRARAA 30

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGACYGYTC TNRSNRYTGA CMGVTAC 27

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGACYGYTC TNRSNRYTGA CMGVTAT 27

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCGCSGCYTC TNRGYATGGA YCGNTAC 27

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATGTGRTAR GGSRNCCAAC AGANGRYAAA 30

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATGTGRTAR GGSRNCCAAC AGANGRYGAA 30

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GYCACCAACN WSTTCATCCT SWNHCTG 27

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ASNSANRAAG SARTAGANGA NRGGRTT 27

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGNTSSTKMT NGSNGTKGTN GGNAA 25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AYCKGTAYCK GTCCANKGWN ATKGC 25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATKKCCSTG GASAGNTAYN TRGC 24

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GWWGGGSAKC CAGCASANGG CRAA 24

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: 15th N is A, G, C, or T
6th, 9th, 10th & 12th Ns are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ARYYTNGCNN TNGCNGAY 18

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: 13th, 15th, 16th & 18th Ns are
each A, G, C, or T
1st, 4th, 6th Ns are inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

NGGNANCCAR CANANNRNRA A 21

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTSNTNRN SATGWSTGTG GANMGNT 27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GAWSNTGMYN ANRTGGWAGG GNANCCA 27

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TAGTGTGTGG AGTCGTGTGG CTGGCTG 27

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AGTCTTGCT GCCACAGGCA TCCAGCG 27

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CAAGCCAGTA AGGCTATGAA GGGCAGCAAG 30

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACAGGACCTG CTGGGCCATC CTGGCGACAC A 31

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
1 * 5 10 15

Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
20 25 30

Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
35 40 45

Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
50 55 60

Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65 70 75 80

Val Val Leu Val His Pro Leu Arg Arg Arg Ile
85 90

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu
1 5 10 15

Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
20 25 30

Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg
35 40 45

Thr Phe Cys Leu Leu Val Val Val Val Val Val
50 55

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
1 5 10 15

Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
20 25 30

Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
35 40 45

Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
50 55 60

Leu Leu Tyr Ser Val Val Val Val Gly Leu Val Gly Asn Cys Leu
65 70 75 80

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
85 90 95

Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
100 105 110

Cys Val Pr

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shozi Fukusumi

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shozi Fukusumi

u Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
180 185 190

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
195 200 205

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
210 215 220

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
225 230 235 240

Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val

	245	250	255
Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg			
260	265	270	
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala			
275	280	285	
Val Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp			
290	295	300	
Pro His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys			
305	310	315	320
His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala			
325	330	335	
Trp Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala			
340	345	350	
Trp Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val			
355	360	365	
Val Ile			
370			

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn			
1	5	10	15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala			
20	25	30	
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val			
35	40	45	
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr			
50	55	60	
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr			
65	70	75	80
Val Val Leu Val His Pro Leu Arg Arg Ile Ser Leu Arg Leu Ser			
85	90	95	

Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu
100 105 110

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
115 120 125

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
130 135 140

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145 150 155 160

Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165 170 175

Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
180 185 190

Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
195 200 205

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
1 5 10 15

Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
20 25 30

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
35 40 45

Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile
50 55 60

Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala
65 70 75 80

Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
85 90 95

Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
100 105 110

Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
115 120 125

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAAC TT CCTCATCGGC 60
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 120
GCCTTCGAGC CACGCGGCTG GGTGTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGCCGGTCA CCGTCTATGT GT CGGTGTT TC ACGCTCACCA CCATCGCAGT GGACCGGTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCCGGCGC ATC 273

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GGCCTGCTGC TGGTCACCTA CCTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGG 60
GTGTCAGTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC 120
TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG 177

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGGCCTCAT CGACCACTCG GGGCCCCAGG GTTTCTGACT TATTTCTGG GCTGCCGCCG	60
GC GGTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CGGGCAACGG GTCGGTGGCT	120
GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG	180
GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCCTG	240
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACCT CCTCATCGC	300
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT	360
GCCTTCGAGC CACGCGGCTG GGTGTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG	420
CAGCCGGTCA CCGTCTATGT GTCGGTGTTA ACGCTCACCA CCATCGCAGT GGACCGCTAC	480
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG	540
CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC	600
GTGGAGCTCA AGCCGCACGA CGTGCACCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC	660
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC	720
ATCCTCCTGT CTTACGTCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC	780
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG	840
GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGCTGCCGC TGCACGTCTT CAACCTGCTG	900
CGGGACCTCG ACCCCCACGC CATCGACCCCT TACGCCTTG GGCTGGTGCA GCTGCTCTGC	960
CACTGGCTCG CCATGAGTTC GGCCTGCTAC AACCCCTTCA TCTACGCCTG GCTGCACGAC	1020
AGCTTCCGCG AGGAGCTGCG CAAACTGTTG GTCGCTTGGC CCCGCAAGAT AGCCCCCCAT	1080
GGCCAGAATA TGACCGTCAG CGTGGTCATC	1110

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 618
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGTACAACG TGACGAATTT CCTCATCGGC 60
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 120
GCCTTCGAGC CACGCCGCTG GGTGTTCGGC GGCAGGCTGT GCCACCTGGT CTTCTTCCTG 180
CAGGCCGGTCA CCGTCTATGT GTCCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGCTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 300
CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 360
GTGGAGCTCA AGCCGCACGA CGTGCACCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 420
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 480
ATCCTCCTGT CTTACGCCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCCGC 540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 600
GTGGTGGTCG TGGTGGTG 618

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTCACTGA GGCTCAGCGC CTACGCGGTG 60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT 120
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTGCTCCC CCTGCTGGCC 240
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC 300

GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360
GTGGTGGTGG TGGTAGTG 378

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser
1 5 10 15

Leu Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Ile
20 25 30

Asn Thr Pro Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe
35 40 45

Gly Lys Gly Met Cys His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu
50 55 60

His Val Ser Ala Leu Thr
65 70

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Glu Pro Ala Asp Leu Phe Trp Lys Asn Leu Asp Leu Pro Thr Phe Ile
1 5 10 15

Leu Leu Asn Ile Leu Pro Leu Leu Ile Ile Ser Val Ala Tyr Val Arg
20 25 30

Val Thr Lys Lys Leu Trp Leu Cys Asn Met Ile Val Asp Val Thr Thr
35 40 45

Glu Gln Tyr Phe Ala Leu Arg Pro Lys Lys Lys Lys Thr Ile Lys Met
50 55 60

Leu Met Leu Val Val Val Leu
65 70

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTCTGTCATG TCATCTTCAA GAACCAGCGA ATGCACTCGG CCACCAGCCT CTTCATCGTC	60
AACCTGGCAG TTGCCGACAT AATGATCACG CTGCTCAACA CCCCCTTCAC TTTGGTTCGC	120
TTTGTGAACA GCACATGGAT ATTTGGGAAG GGCATGTGCC ATGTCAGCCG CTTTGCCCAG	180
TACTGCTCAC TGCACGTCTC AGCACTGACA	210

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GAGCCAGCTG ACCTCTTCTG GAAGAACCTG GACTTGCCCA CCTTCATCCT GCTAACATC	60
CTGCCCTCC TCATCATCTC TGTGGCCTAC GTTCGTGTGA CCAAGAACT GTGGCTGTGT	120
AATATGATTG TCGATGTGAC CACAGAGCAG TACTTGCCC TGCGGCCAA AAAGAAGAAG	180
ACCATCAAGA TGTTGATGCT GGTGGTAGTC CTC	213

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala Trp Val Val Cys
1 5 10 15

Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu Pro Thr Ala Val
20 25 30

Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val Cys Tyr Asp Leu
35 40 45

Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr Gly Met Ala Leu
50 55 60

Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu Leu Ala Cys Tyr
65 70 75 80

Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly Pro Ala Gly Pro
85 90 95

Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met Ala Val Val Val
100 105 110

Ala Ala Val
115

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Met Glu Gln Asp Asn Gly Thr Ile Gln Ala Pro Gly Leu Pro Pro Thr
1 5 10 15

Thr Cys Val Tyr Arg Glu Asp Phe Lys Arg Leu Leu Leu Thr Pro Val
20 25 30

Tyr Ser Val Val Leu Val Val Gly Leu Pro Leu Asn Ile Cys Val Ile
35 40 45

Ala Gln Ile Cys Ala Ser Arg Arg Thr Leu Thr Arg Ser Ala Val Tyr
50 55 60

Thr Leu Asn Leu Ala Leu Ala Asp Leu Met Tyr Ala Cys Ser Leu Pro
65 70 75 80

Leu Leu Ile Tyr Asn Tyr Ala Arg Gly Asp His Trp Pro Phe Gly Asp
85 90 95

Leu Ala Cys Arg Phe Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
100 105 110

Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
115 120 125

Cys His Pro Leu Ala Ser Trp His Lys Arg Gly Gly Arg Arg Ala Ala
130 135 140

Trp Val Val Cys Gly Val Val Trp Leu Ala Val Thr Ala Gln Cys Leu
145 150 155 160

Pro Thr Ala Val Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
165 170 175

Cys Tyr Asp Leu Ser Pro Pro Ile Leu Ser Thr Arg Tyr Leu Pro Tyr
180 185 190

Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ile Ala Leu
195 200 205

Leu Ala Cys Tyr Cys Arg Met Ala Arg Arg Leu Cys Arg Gln Asp Gly
210 215 220

Pro Ala Gly Pro Val Ala Gln Glu Arg Arg Ser Lys Ala Ala Arg Met
225 230 235 240

Ala Val Val Val Ala Ala Val Phe Ala Ile Ser Phe Leu Pro Phe His
245 250 255

Ile Thr Lys Thr Ala Tyr Leu Ala Val Arg Ser Thr Pro Gly Val Ser
260 265 270

Cys Pro Val Leu Glu Thr Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
275 280 285

Phe Ala Ser Val Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
290 295 300

Gln Gln Lys Phe Arg Arg Gln Pro His Asp Leu Leu Gln Arg Leu Thr
305 310 315 320

Ala Lys Trp Gln Arg Gln Arg Val
325

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GCTTCCTGGC ACAAGCGTGG AGGTGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG 60
CTGGCTGTGA CAGCCCAGTG CCTGCCACG GCAGTCTTG CTGCCACAGG CATCCAGCGC 120
AACCGCACTG TGTGCTACGA CCTGAGCCA CCCATCCTGT CTACTCGCTA CCTGCCCTAT 180
GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTCA TAGCCTTACT GGCTTGTTAT 240
TGTCGCATGG CCCGCCGCCT GTGTCGCCAG GATGGCCCAG CAGGTCCCTGT GGCCCAAGAG 300
CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shoji Fukusumi

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shuji Hinuma
Masaki Hosoya
Ryo Fujii
Tetsuya Ohtaki
Shoji Fukusumi

T CGGTGGTGCT GGTGGTCGGC 120

CTGCCACTGA ACATCTGCGT CATTGCCAG ATCTGCGCAT CCCGCCGGAC CCTGACCCGT 180
TCCGCTGTGT ACACCCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TTCACTACCC 240
CTACTTATCT ATAACCTACGC CAGAGGGGAC CACTGCCCT TCGGAGACCT CGCCTGCCGC 300
TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTCTT CACCTGCATT 360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT 420

CGCCGTGCTG	CTTGGGTAGT	GTGTGGAGTC	GTGTGGCTGG	CTGTGACAGC	CCAGTGCCTG	480
CCCACGGCAG	TCTTGCTGC	CACAGGCATC	CAGCGCAACC	GCACTGTGTG	CTACGACCTG	540
AGCCCACCCA	TCCTGTCTAC	TCGCTACCTG	CCCTATGGTA	TGGCCCTCAC	GGTCATCGGC	600
TTCTTGCTGC	CCTTCATAGC	CTTACTGGCT	TGTTATTGTC	GCATGGCCCG	CCGCCTGTGT	660
CGCCAGGATG	GCCCAGCAGG	TCCTGTGGCC	CAAGAGCGGC	GCAGCAAGGC	GGCTCGTATG	720
GCTGTGGTGG	TGGCAGCTGT	CTTGCCATC	AGCTTCCTGC	CTTTCCACAT	CACCAAGACA	780
GCCTACTTGG	CTGTGCGCTC	CACGCCCGGT	GTCTCTTGCC	CTGTGCTGGA	GACCTTCGCT	840
GCTGCCTACA	AAGGCACTCG	GCCCTTCGCC	AGTGTCAACA	GTGTTCTGGA	CCCCATTCTC	900
TTCTACTTCA	CACAAACAGAA	GTTCCGGCGG	CAACCCCACG	ATCTCTTACA	GAGGCTCACA	960
GCCAAGTGGC	AGAGGCAGAG	AGTC				984

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Ala	Ala	Met	Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	Val	His	Ser	Arg	Arg
1				5					10					15	
Ser	Ser	Ser	Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	Gly	Val	Gly	Phe
									20		25			30	
Ile	Trp	Ala	Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	His	Gln
								35		40			45		
Arg	Leu	Phe	His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	Gln	Trp
								50		55		60			
Pro	Asn	Lys	Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe
								65		70		75		80	
Gly	Tyr	Leu	Leu	Pro	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	
								85		90		95			
Leu	Asn	His	Leu	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Ser	Glu	
								100		105		110			
Ala	Ser	Lys	Lys	Lys	Thr	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val
								115		120		125			

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GCCGCGATGT CTGTGGATCG CTACGTGGCC ATTGTGCACT CGCGGCGCTC CTCCTCCCTC	60
AGGGTGTCCC GCAACGCACT GCTGGGCGTG GGCTTCATCT GGGCGCTGTC CATGCCATG	120
GCCTCGCCGG TGGCCTACCA CCAGCGTCTT TTCCATCGGG ACAGCAACCA GACTTCTGC	180
TGGGAGCAGT GGCCCAACAA GCTCCACAAG AAGGCTTACG TGGTGTGCAC TTTCGTCTTT	240
GGGTACCTTC TGCCCTTACT GCTCATCTGC TTTGCTATG CCAAGGT CCT TAATCATCTG	300
CATAAAAAGC TGAAAAACAT GTCAAAAAAG TCTGAAGCAT CCAAGAAAAA GACTGCACAG	360
ACCGTCCTGG TGGTCGTTGT AGTA	384

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Val Leu Trp Phe Phe Gly Phe Ser Ile Lys Arg Thr Pro Phe Ser Val			
1	5	10	15
Tyr Phe Leu His Leu Ala Ser Ala Asp Gly Ala Tyr Leu Phe Ser Lys			
20	25	30	
Ala Val Phe Ser Leu Leu Asn Ala Gly Gly Phe Leu Gly Thr Phe Ala			
35	40	45	
His Tyr Val Arg Ser Val Ala Arg Val Leu Gly Leu Cys Ala Phe Val			
50	55	60	
Ala Gly Val Ser Leu Leu Pro			

65

70

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GTGCTCTGGT TCTTCGGCTT CTCCATCAAG AGGACCCCCT TCTCCGTCTA CTTCCTGCAC	60
CTGGCCAGCG CCGACGGCGC CTACCTCTTC AGCAAGGCCG TGTTCTCCCT GCTGAACGCC	120
GGCGGCTTCC TGGGCACCTT CGCCCACTAT GTGCGCAGCG TGGCCCGGGT GCTGGGGCTC	180
TGCGCCTTCG TGGCGGGCGT GAGCCTCCTG CCGGC	215

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Glu Leu Ala Met Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro			
1	5	10	15

Glu Pro Pro Ala Pro Glu Ser Arg Pro Leu Phe Gly Ile Gly Val Glu		
20	25	30

Asn Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val		
35	40	45

Leu Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly		
50	55	60

Lys Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala			
65	70	75	80

Asp Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr		
85	90	95

Ala Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His		
100	105	110

Tyr Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala
115 120 125

Met Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser
130 135 140

Ser Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp
145 150 155 160

Ala Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr His Gln Arg Leu
165 170 175

Phe His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu Gln Trp Pro Asn
180 185 190

Lys Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr
195 200 205

Leu Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn
210 215 220

His Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser
225 230 235 240

Lys Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Phe Gly
245 250 255

Ile Ser Trp Leu Pro His His Val Val His Leu Trp Ala Glu Phe Gly
260 265 270

Ala Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His
275 280 285

Cys Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe
290 295 300

Leu Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys His
305 310 315 320

Val Cys Asp Glu Ser Pro Arg Ser Glu Thr Lys Glu Asn Lys Ser Arg
325 330 335

Met Asp Thr Pro Pro Ser Thr Asn Cys Thr His Val
340 345

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

(C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGGAACCTGG CTATGGTGAA CCTCAGTGAA GGGATGGGA GCGACCCAGA GCCGCCAGCC	60
CCGGAGTCCA GGCGCTCTT CGGCATTGGC GTGGAGAACT TCATTACGCT GGTAGTGT	120
GGCCTGATT TCGCGATGGG CGTGCTGGC AACAGCCTGG TGATCACCGT GCTGGCGCGC	180
AGCAAACCAG GCAACCCCCG CAGCACCAACC AACCTGTTA TCCTCAATCT GAGCATCGCA	240
GACCTGGCCT ACCTGCTCTT CTGCATCCCT TTTCAGGCCA CCGTGTATGC ACTGCCACC	300
TGGGTGCTGG GCGCCTTCAT CTGCAAGTTT ATACACTACT TCTTCACCGT GTCCATGCTG	360
GTGAGCATCT TCACCCCTGGC CGCGATGTCT GTGGATCGCT ACGTGGCCAT TGTGCACTCG	420
CGGCGCTCCT CCTCCCTCAG GGTGTCCCAG AACGCAGTGC TGGGCGTGGG CTTCATCTGG	480
GCGCTGTCCA TCGCCATGGC CTCGCCGGTG GCCTACCACC AGCGTCTTT CCATCGGGAC	540
AGCAACCAGA CCTTCTGCTG GGAGCAGTGG CCCAACAAAGC TCCACAAGAA GGCTTACGTG	600
GTGTGCACTT TCGTCTTG GTACCTTCTG CCCTTACTGC TCATCTGCTT TTGCTATGCC	660
AAGGTCTTA ATCATCTGCA TAAAAAGCTG AAAAACATGT CAAAAAAAGTC TGAAGCATTCC	720
AAGAAAAAGA CTGCACAGAC CGTCCTGGTG GTCGTTGTAG TATTTGGCAT ATCCTGGCTG	780
CCCCATCATG TCGTCCACCT CTGGGCTGAG TTTGGAGCCT TCCCAGTGAC GCCAGCTTCC	840
TTCTTCTTCA GAATCACCGC CCATTGCCTG GCATACAGCA ACTCCTCAGT GAACCCCATC	900
ATATATGCCT TTCTCTCAGA AAACCTCCGG AAGGCGTACA AGCAAGTGT CAAGTGTCA	960
GTGGCGATG AATCTCCACG CAGTGAAACT AAGGAAAACA AGAGCCGGAT GGACACCCCG	1020
CCATCCACCA ACTGCACCCA CGTG	1044

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Leu	Leu	Thr	Leu	His	Pro	Val	Trp	Ser	Gln	Lys	His	Arg	Thr	Ser	His
1					5				10					15	

Trp	Ala	Ser	Arg	Val	Val	Leu	Gly	Val	Trp	Leu	Ser	Ala	Thr	Ala	Phe
	20							25					30		
Ser	Val	Pro	Tyr	Leu	Val	Phe	Arg	Glu	Thr	Tyr	Asp	Asp	Arg	Lys	Gly
	35					40							45		
Arg	Val	Thr	Cys	Arg	Asn	Asn	Tyr	Ala	Val	Ser	Thr	Asp	Trp	Glu	Ser
	50				55					60					
Lys	Glu	Met	Gln	Thr	Val	Arg	Gln	Trp	Ile	His	Ala	Thr	Cys	Phe	Ile
	65				70				75				80		
Ser	Arg	Phe	Ile	Leu	Gly	Phe	Leu	Leu	Pro	Phe	Leu	Val	Ile	Gly	Phe
		85					90						95		
Cys	Tyr	Glu	Arg	Val	Ala	Arg	Lys	Met	Lys	Glu	Arg	Gly	Leu	Phe	Lys
		100				105						110			
Ser	Ser	Lys	Pro	Phe	Lys	Val	Thr	Met	Thr	Ala	Val	Ile			
		115				120					125				

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CTTCTCACCC	TTCACCCAGT	GTGGTCCCAA	AAGCACCGAA	CCTCACACTG	GGCTTCCAGA	60
GTCGTTCTGG	GAGTCTGGCT	CTCTGCCACT	GCCTTCAGCG	TGCCCTATT	GGTTTCAGG	120
GAGACATATG	ATGACCGTAA	AGGAAGAGTG	ACCTGCAGAA	ATAACTACGC	TGTGTCCACT	180
GACTGGGAAA	GCAAAGAGAT	GCAAACAGTA	AGACAATGGA	TTCATGCCAC	CTGTTTCATC	240
AGCCGCTTCA	TACTGGGCTT	CCTTCTGCCT	TTCTTAGTCA	TTGGCTTTG	TTATGAAAGA	300
GTAGCCCGCA	AGATGAAAGA	GAGGGGCCTC	TTTAAATCCA	GCAAACCCTT	CAAAGTCACG	360
ATGACTGCTG	TTATCTC					377

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Phe Lys Ile Val Lys Pro Leu Ser Thr Ser Phe Ile Gln Ser Val Asn
1 5 10 15

Tyr Ser Lys Leu Val Ser Leu Val Val Trp Leu Leu Met Leu Leu Leu
20 25 30

Ala Val Pro Asn Val Ile Leu Thr Asn Gln Arg Val Lys Asp Val Thr
35 40 45

Gln Ile Lys Cys Met Glu Leu Lys Asn Glu Leu Gly Arg Gln Trp His
50 55 60

Lys Ala Ser Asn Tyr Ile Phe Val Gly Ile Phe Trp Leu Val Phe Leu
65 70 75 80

Leu Leu Ile Ile Phe Tyr Thr Ala Ile Thr Arg Lys Ile Phe Lys Ser
85 90 95

His Leu Lys Ser Arg Lys Asn Ser Ile Ser Val Lys Lys Ser Ser
100 105 110

Arg Asn Ile Phe Ser Ile Val
115

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCAAGATTG TGAAGCCCC TTCCACGTCC TTCATCCAGT CTGTGAACTA CAGCAAACTC 60

GTCTCGCTGG TGGTCTGGTT GCTCATGCTC CTCCTCGCCG TCCCCAACGT CATTCTCAC 120

AACCAGAGAG TTAAGGACGT GACGCAGATA AAATGCATGG AACTTAAAAA CGAACTGGGC 180

CGCCAGTGGC ACAAGGCGTC AAACTACATC TTTGTGGCA TTTCTGGCT TGTGTTCC 240

TTGCTAATCA TTTTCTACAC TGCTATCACC AGGAAAATCT TTAAGTCCA CCTGAAATCC 300
AGAAAGAATT CCATCTCGGT CAAAAAGAAA TCTAGCCGCA ACATCTTCAG CATCGTG 357

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Val Asp Leu Leu Ala Ala Leu Thr Leu Met Pro Leu Ala Met Leu Ser
1 5 10 15

Ser Ser Ala Leu Phe Asp His Ala Leu Phe Gly Glu Val Ala Cys Arg
20 25 30

Leu Tyr Leu Phe Leu Ser Val Cys Phe Val Ser Leu Ala Ile Leu Ser
35 40 45

Val Ser Ala Ile Asn Val Glu Arg Tyr Tyr Tyr Val Val His Pro Met
50 55 60

Arg Tyr Glu Val Arg Met Lys Leu Gly Leu Val Ala Ser Val Leu Val
65 70 75 80

Gly Val Trp Val Lys Ala Leu Ala Met Ala Ser Val Pro Val Leu Gly
85 90 95

Arg Val Ser Trp Glu Glu Gly Pro Pro Ser Val Pro Pro Gly Cys Ser
100 105 110

Leu Gln Trp Ser His Ser Ala Tyr Cys Gln Leu Phe Val Val Val Phe
115 120 125

Ala Val Leu Tyr Phe Leu Leu Pro Leu Leu Ile Leu Val Val Tyr
130 135 140

Cys Ser Met Phe Arg Val Ala Arg Val Ala Ala Met Gln His Gly Pro
145 150 155 160

Leu Pro Thr Trp Met Glu Thr Pro Arg Gln Arg Ser Glu Ser Leu Ser
165 170 175

Ser Arg Ser Thr Met Val Thr Ser Ser Gly Ala Pro Gln Thr Thr Pro
180 185 190

His Arg Thr Phe Gly Gly Lys Ala Ala Val Val Leu Leu Ala Val
195 200 205

Gly Gly Gln Phe Leu Leu Cys Trp Leu Pro Tyr Phe Ser Phe His Leu
210 215 220

Tyr Val Ala Leu Ser Ala Gln Pro Ile Ala Ala Gly Gln Val Glu Asn
225 230 235 240

Val Val Thr Trp Ile Gly Tyr Phe Cys Phe Thr Ser
245 250

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GTGGACCTGC TGGCTGCCCT GACCCTCATG CCTCTGGCCA TGCTCTCCAG CTCCGCCCTC 60
TTTGACCACG CCCTCTTGG GGAGGTGGCC TGCCGCCTCT ACTTGTTCCCT GAGCGTCTGC 120
TTTGTCAAGCC TGGCCATCCT CTCGGTGTCC GCCATCAATG TGGAGCGCTA CTATTATGTG 180
GTCCACCCCA TGCGCTATGA GGTGCGCATG AAACCTGGGGC TGGTGGCCTC TGTGCTGGTG 240
GGCGTGTGGG TGAAGGCCCT GGCCATGGCT TCTGTGCCAG TGTGGGAAG GGTGTCCCTGG 300
GAGGAAGGCC CTCCCAGTGT CCCCCAGGC TGTTCACTCC AATGGAGCCA CAGTGCCTAC 360
TGCCAGCTTT TCGTGGTGGT CTTGCCGTC CTCTACTTCC TGCTGCCCT GCTCCTCATC 420
CTTGTGGTCT ACTGCAGCAT GTTCCGGGTG GCTCGTGTGG CTGCCATGCA GCACGGGCCG 480
CTGCCAACGT GGATGGAGAC GCCCCGGCAA CGCTCCGAGT CTCTCAGCAG CCGCTCCACT 540
ATGGTCACCA GCTCGGGGGC CCCGCAGACC ACCCCTCACC GGACGTTGG CGGAGGGAAAG 600
GCAGCAGTGG TCCTCCTGGC TGTGGGAGGA CAGTTCTGC TCTGTTGGTT GCCCTACTTC 660
TCCTTCCACC TCTATGTGGC CCTGAGCGCT CAGCCCCATTG CAGCGGGGCA GGTGGAGAAC 720
GTGGTGACCT GGATTGGCTA CTTCTGCTTC ACCTCC 756

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Ala Asp Val Leu Val Thr Ala Ile Cys Leu Pro Ala Ser Leu Leu Val
1 5 10 15

Asp Ile Thr Glu Ser Trp Leu Phe Gly His Ala Leu Cys Lys Val Ile
20 25 30

Pro Tyr Leu Gln Ala Val Ser Val Ser Val Val Val Leu Thr Leu Ser
35 40 45

Ser Ile Ala Leu Asp Arg Trp Tyr Ala Ile Cys His Pro Leu Leu Phe
50 55 60

Lys Ser Thr Ala Arg Arg Ala Arg Gly Ser Ile Leu Gly Ile Trp Ala
65 70 75 80

Val Ser Leu Ala Val Met Val Pro Gln Ala Ala Val Met Glu Cys Ser
85 90 95

Ser Val Leu Pro Glu Leu Ala Asn Arg Thr Arg Leu Leu Ser Val Cys
100 105 110

Asp Glu Arg Trp Ala Asp Asp Leu Tyr Pro Lys Ile Tyr His Ser Cys
115 120 125

Phe Phe Ile Val Thr Tyr Leu Ala Pro Leu Gly Leu Met Ala Met Ala
130 135 140

Tyr Phe Gln Ile Phe Arg Lys Leu Trp Gly Arg Gln Ile Pro Gly Thr
145 150 155 160

Thr Ser Ala Leu Val Arg Asn Trp Lys Arg Pro Ser Asp Gln Leu Asp
165 170 175

Asp Gln Gly Gln Gly Leu Ser Ser Glu Pro Gln Pro Arg Ala Arg Ala
180 185 190

Phe Leu Ala Glu Val Lys Gln Met Arg Ala Arg Arg Lys Thr Ala Lys
195 200 205

Met Leu Met Val Val Leu Leu Val Phe Ala Leu Cys Tyr Leu Pro Ile
210 215 220

Ser Val Leu Asn Val Leu Lys Arg Val Phe Gly Met Phe Arg Gln Ala
225 230 235 240

Ser Asp Arg Glu Ala Ile Tyr Ala Cys Phe Thr Phe Ser His Trp Leu
245 250 255

Val Tyr Ala Asn Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GCCGATGTGC	TGGTGACAGC	CATCTGCCTG	CCGGCCAGTC	TGCTGGTAGA	CATCACGGAA	60
TCCTGGCTCT	TTGGCCATGC	CCTCTGCAAG	GTCATCCCCT	ATCTACAGGC	CGTGTCCGTG	120
TCAGTGGTCG	TGCTGACTCT	CAGCTCCATC	GCCCTGGACC	GCTGGTACGC	CATCTGCCAC	180
CCGCTGTTGT	TCAAGAGCAC	TGCCCGGCGC	GCCCGCGGCT	CCATCCTCGG	CATCTGGCG	240
GTGTCGCTGG	CTGTCATGGT	GCCTCAGGCT	GCTGTCATGG	AGTGTAGCAG	CGTGCTGCC	300
GAGCTGGCCA	ACCGCACCCG	CCTCCTGTCT	GTCTGTGATG	AGCGCTGGC	AGACGACCTG	360
TACCCCAAGA	TCTACCACAG	CTGCTTCTTC	ATTGTCACCT	ACCTGGCCCC	ACTGGGCCTC	420
ATGGCCATGG	CCTATTCCA	GATCTTCCGC	AAGCTCTGGG	GCCGCCAGAT	CCCCGGCACC	480
ACCTCGGCC	TGGTGCGCAA	CTGGAAGCGG	CCCTCAGACC	AGCTGGACGA	CCAGGGCCAG	540
GGCCTGAGCT	CAGAGCCCCA	GCCCCGGGCC	CGCGCCTTCC	TGGCCGAGGT	GAAACAGATG	600
CGAGCCCGGA	GGAAGACGGC	CAAGATGCTG	ATGGTGGTGC	TGCTGGTCTT	CGCCCTCTGC	660
TACCTGCCCA	TCAGTGTCT	CAACGTCTC	AAGAGGGTCT	TCGGGATGTT	CCGCCAAGCC	720
AGCGACCGAG	AGGCCATCTA	CGCCTGCTTC	ACCTTCTCCC	ACTGGCTGGT	GTACGCCAAC	780
AGCGCCGCC						789

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328
- (B) TYPE: Amino acid
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Met Glu Trp Asp Asn Gly Thr Gly Gln Ala Leu Gly Leu Pro Pro Thr
1 5 10 15

Thr Cys Val Tyr Arg Glu Asn Phe Lys Gln Leu Leu Leu Pro Pro Val
20 25 30

Tyr Ser Ala Val Leu Ala Ala Gly Leu Pro Leu Asn Ile Cys Val Ile
35 40 45

Thr Gln Ile Cys Thr Ser Arg Arg Ala Leu Thr Arg Thr Ala Val Tyr
50 55 60

Thr Leu Asn Leu Ala Leu Ala Asp Leu Leu Tyr Ala Cys Ser Leu Pro
65 70 75 80

Leu Leu Ile Tyr Asn Tyr Ala Gln Gly Asp His Trp Pro Phe Gly Asp
85 90 95

Phe Ala Cys Arg Leu Val Arg Phe Leu Phe Tyr Ala Asn Leu His Gly
100 105 110

Ser Ile Leu Phe Leu Thr Cys Ile Ser Phe Gln Arg Tyr Leu Gly Ile
115 120 125

Cys His Pro Leu Ala Pro Trp His Lys Arg Gly Gly Arg Arg Ala Ala
130 135 140

Trp Leu Val Cys Val Thr Val Trp Leu Ala Val Thr Thr Gln Cys Leu
145 150 155 160

Pro Thr Ala Ile Phe Ala Ala Thr Gly Ile Gln Arg Asn Arg Thr Val
165 170 175

Cys Tyr Asp Leu Ser Pro Pro Ala Leu Ala Thr His Tyr Met Pro Tyr
180 185 190

Gly Met Ala Leu Thr Val Ile Gly Phe Leu Leu Pro Phe Ala Ala Leu
195 200 205

Leu Ala Cys Tyr Cys Leu Leu Ala Cys Arg Leu Cys Arg Gln Asp Gly
210 215 220

Pro Ala Glu Pro Val Ala Gln Glu Arg Arg Gly Lys Ala Ala Arg Met
225 230 235 240

Ala Val Val Val Ala Ala Ala Phe Ala Ile Ser Phe Leu Pro Phe His
245 250 255

Ile Thr Lys Thr Ala Tyr Leu Ala Val Gly Ser Thr Pro Gly Val Pro
260 265 270

Cys Thr Val Leu Glu Ala Phe Ala Ala Ala Tyr Lys Gly Thr Arg Pro
275 280 285

Phe Ala Ser Ala Asn Ser Val Leu Asp Pro Ile Leu Phe Tyr Phe Thr
290 295 300

Gln Lys Lys Phe Arg Arg Arg Pro His Glu Leu Leu Gln Lys Leu Thr
305 310 315 320

Ala Lys Trp Gln Arg Gln Gly Arg
325

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE

- (C) IDENTIFICATION METHOD: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATGGAATGGG ACAATGGCAC AGGCCAGGCT CTGGGTTGC CACCCACCAC CTGTGTCTAC	60
CGCGAGAACT TCAAGCAACT GCTGCTGCCA CCTGTGTATT CGGCGGTGCT GGCGGCTGGC	120
CTGCCGCTGA ACATCTGTGT CATTACCCAG ATCTGCACGT CCCGCCGGGC CCTGACCCGC	180
ACGGCCGTGT ACACCCCTAAA CCTTGCTCTG GCTGACCTGC TATATGCCTG CTCCCTGCC	240
CTGCTCATCT ACAACTATGC CCAAGGTGAT CACTGGCCCT TTGGCGACTT CGCCTGCCGC	300
CTGGTCCGCT TCCTCTTCTA TGCCAACCTG CACGGCAGCA TCCTCTTCCT CACCTGCATC	360
AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCGCTGGCCC CCTGGCACAA ACGTGGGGC	420
CGCCGGGCTG CCTGGCTAGT GTGTGTAACC GTGTGGCTGG CCGTGACAAC CCAGTGCCTG	480
CCCACAGCCA TCTTCGCTGC CACAGGCATC CAGCGTAACC GCACTGTCTG CTATGACCTC	540
AGCCCGCCTG CCCTGGCCAC CCACTATATG CCCTATGGCA TGGCTCTCAC TGTCATCGC	600
TTCCTGCTGC CCTTGCTGC CCTGCTGGCC TGCTACTGTC TCCTGGCCTG CCGCCTGTGC	660
CGCCAGGATG GCCCGGCAGA GCCTGTGGCC CAGGAGCGGC GTGGCAAGGC GGCCCGCATG	720
GCCGTGGTGG TGGCTGCTGC CTTGCCATC AGCTTCCTGC CTTTCACAT CACCAAGACA	780
GCCTACCTGG CAGTGGGCTC GACGCCGGC GTCCCCTGCA CTGTATTGGA GGCCTTGCA	840
CGGGCCTACA AAGGCACGCG GCCGTTGCC AGTGCCAAC A GCGTGCTGGA CCCCATCCTC	900
TTCTACTTCA CCCAGAAGAA GTTCCGCCGG CGACCACATG AGCTCCTACA GAAACTCACA	960

GCCAAATGGC AGAGGCAGGG TCGC

984

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ACAGCCATCT TCGCTGCCAC AGGCAT 26

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

AGACAGTAGC AGGCCAGCAG GGCAGCAAA 29

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGTGYGYSA TYGCNNTKGA YMGSTAC 27

(2) INFORMATION FOR SEQ ID NO: 61:

Cont
D1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(iii) FEATURES: N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AKGWAGWAGG GCAGCCAGCA GANSRYGAA 29